

**Amendments to the claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1-31 (canceled)

Claim 32 (currently amended): A method for identifying single nucleotide polymorphic sites in a genome of a species of interest, comprising:

- (a) isolating a plurality of DNA fragments from the genome of a population of individual representatives of the species of interest, wherein each fragment corresponds to a location of the genome and the fragments are between about 0.1 kb and 10.0 kb;
- (b) sequencing the DNA fragments to determine the nucleotide sequences of each fragment, and
- (c) comparing the sequence of each fragment to corresponding fragments from other individual representatives of the species of interest to identify sites of sequence variation, wherein the species of interest is a mammal.

Claim 33 (previously presented): A method according to claim 32, wherein the plurality of DNA fragments is from a population of between 10 to 100 individual representatives of the same species.

Claim 34 (previously presented): A method according to claim 32, wherein the plurality of DNA fragments is from a population of between 100 to 1000 individual representatives of the same species.

Claim 35 (previously presented): A method according to claim 32, wherein the plurality of DNA fragments is from a population of between 100 and 10,000 individual representatives of the same species.

Claim 36 (previously presented): A method according to claim 32, wherein the fragments are between 0.5 kb and 3.0 kb.

Claim 37 (previously presented): A method according to claim 32, wherein the fragments are sequenced by dideoxy sequencing.

Claim 38 (previously presented): A method according to claim 32, wherein the fragments are isolated by amplification using oligonucleotide primers.

Claim 39 (currently amended): A method for determining allelic frequency at a single nucleotide polymorphic site, comprising:

(a) isolating a plurality of DNA fragments from a population of two or more individual representatives of a species of interest, wherein each fragment corresponds to a location of the genome and the fragments are between about 0.1 kb and 10.0 kb;

(b) sequencing the DNA fragments to determine the nucleotide sequences of each fragment;

(c) comparing the sequence of each fragment to corresponding DNA fragments from different individual representatives of the species of interest and identifying single nucleotide polymorphic sites having at least two alleles,

(d) determining the base identity of each allele present in the location of the genome, and

(e) calculating the allelic frequency for each allele by dividing the frequency at which each allele appears in the sample set by the total number of individuals, wherein the species of interest is a mammal.

Claim 40 (previously presented): A method according to claim 39, wherein the plurality of DNA fragments is from a population of between 10 to 100 individual representatives of the same species.

Claim 41 (previously presented): A method according to claim 39, wherein the plurality of DNA fragments is from a population of between 100 to 1000 individual representatives of the same species.

Claim 42 (previously presented): A method according to claim 39, wherein the plurality of DNA fragments is from a population of between 100 and 10,000 individual representatives of the same species.

Claim 43 (previously presented): A method according to claim 39, wherein the fragments are between 0.5 kb and 3.0 kb.

Claim 44 (previously presented): A method according to claim 39, wherein the fragments are sequenced by dideoxy sequencing.

Claim 45 (previously presented): A method according to claim 39, wherein the fragments are isolated by amplification using oligonucleotide primers.

Claim 46 (new): A method according to claim 32, wherein the method is used to identify a mammal.

Claim 47 (new): A method according to claim 32, wherein the method is used to determine parentage of the mammal.

Claim 48 (new): A method according to claim 32, wherein the mammal is selected from the group consisting of human, non-human primates, dogs, cats, cattle, sheep and horses.

Claim 49 (new): A method according to claim 47, wherein the mammal is a horse.

Claim 50 (new): A method according to claim 46, wherein the mammal is a horse.

Claim 51 (new): A method according to claim 32, wherein the mammal is a human.

Claim 52 (new): A method according to claim 32, wherein the mammal is a horse.

Claim 53 (new): A method according to claim 39, wherein the mammal is selected from the group consisting of human, non-human primates, dogs, cats, cattle, sheep and horses.

Claim 54 (new): A method according to claim 39, wherein the mammal is a human.

Claim 55 (new): A method according to claim 39, wherein the mammal is a horse.